#11

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/492,361

DATE: 06/26/2001
TIME: 07:44:09

Input Set : A:\2815-0127P.ST25.txt
Output Set: N:\CRF3\06262001\I492361.raw

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 3 <110> APPLICANT: JENISCH, Thomas J.
 5 <120> TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
 6        POTASSIUM CHANNELS
 8 <130> FILE REFERENCE: 2815-127P
10 <140> CURRENT APPLICATION NUMBER: 09/492,361
11 <141> CURRENT FILING DATE: 2000-01-27
13 <160> NUMBER OF SEQ ID NOS: 41
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2335
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
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24 <222> LOCATION: (1)..(2335)
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (83)..(2170)
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33 cgcccccagc ccggcgccgc cc atg gcc gag gcc ccc ccg cgc cgc ctc ggc  112
34                         Met Ala Glu Ala Pro Pro Arg Arg Leu Gly
35                          1               5                   10
37 ctg ggt ccc ccg ccc ggg gac gcc ccc cgc gcg gag cta gtg gcg ctc  160
38 Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu
39                 15                  20                  25
41 acg gcc gtg cag agc gaa cag ggc gag gcg ggc ggg ggc ggc tcc ccg  208
42 Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro
43             30                  35                  40
45 cgc cgc ctc ggc ctc ctg ggc agc ccc ctg ccg ccg ggc gcg ccc ctc  256
46 Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu
47             45                  50                  55
49 cct ggg ccg ggc tcc ggc tcg ggc tcc gcc tgc ggc cag cgc tcc tcg  304
50 Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser
51         60                  65                  70
53 gcc gcg cac aag cgc tac cgc cgc ctg cag aac tgg gtc tac aac gtg  352
54 Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val
55 75                  80                  85                  90
57 ctg gag cgg ccc cgc ggc tgg gcc ttc gtc tac cac gtc ttc ata ttt  400
58 Leu Glu Arg Pro Arg Gly Trp Ala Phe Val Tyr His Val Phe Ile Phe
59                 95                  100                 105
61 ttg ctg gtc ttc agc tgc ctg gtg ctg tct gtg ctg tcc act atc cag  448
62 Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Leu Ser Thr Ile Gln
63             110                 115                 120
65 gag cac cag gaa ctt gcc aac gag tgt ctc ctc atc ttg gaa ttc gtg  496
66 Glu His Gln Glu Leu Ala Asn Glu Cys Leu Leu Ile Leu Glu Phe Val
67         125                 130                 135
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69  atg atc gtg gtt ttc ggc ttg gag tac atc gtc cgg gtc tgg tcc gcc     544
70  Met Ile Val Val Phe Gly Leu Glu Tyr Ile Val Arg Val Trp Ser Ala
71      140                 145                 150
73  gga tgc tgc tgc cgc tac cga gga tgg cag ggt cgc ttc cgc ttt gcc     592
74  Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala
75  155                 160                 165                 170
77  aga aag ccc ttc tgt gtc atc gac ttc atc gtg ttc gtg gcc tcg gtg     640
78  Arg Lys Pro Phe Cys Val Ile Asp Phe Ile Val Phe Val Ala Ser Val
79                  175                 180                 185
81  gcc gtc atc gcc gcg ggt acc cag ggc aac atc ttc gcc acg tcc gcg     688
82  Ala Val Ile Ala Ala Gly Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala
83          190                 195                 200
85  ctg cgc agc atg cgc ttc ctg cag atc ctg cgc atg gtg cgc atg gac     736
86  Leu Arg Ser Met Arg Phe Leu Gln Ile Leu Arg Met Val Arg Met Asp
87          205                 210                 215
89  cgc cgc ggc ggc acc tgg aag ctg ctg ggc tca gtg gtc tac gcg cat     784
90  Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val Tyr Ala His
91      220                 225                 230
93  agc aag gag ctg atc acc gcc tgg tac atc ggg ttc ctg gtg ctc atc     832
94  Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile
95  235                 240                 245                 250
97  ttc gcc tcc ttc ctg gtc tac ctg gcc gag aag gac gcc aac tcc gac     880
98  Phe Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp
99                  255                 260                 265
101 ttc tcc tcc tac gcc gac tcg ctc tgg tgg ggg acg att aca ttg aca     928
102 Phe Ser Ser Tyr Ala Asp Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr
103                 270                 275                 280
105 acc atc ggc tat ggt gac aag aca ccg cac aca tgg ctg ggc agg gtc     976
106 Thr Ile Gly Tyr Gly Asp Lys Thr Pro His Thr Trp Leu Gly Arg Val
107         285                 290                 295
109 ctg gct gct ggc ttc gcc tta ctg ggc atc tct ttc ttt gcc ctg cct     1024
110 Leu Ala Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro
111     300                 305                 310
113 gcc ggc atc cta ggc tcc ggc ttt gcc ctg aag gtc cag gag cag cac     1072
114 Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln Glu Gln His
115 315                 320                 325                 330
117 cgg cag aag cac ttc gag aag cgg agg atg ccg gca gcc aac ctc atc     1120
118 Arg Gln Lys His Phe Glu Lys Arg Arg Met Pro Ala Ala Asn Leu Ile
119                 335                 340                 345
121 cag gct gcc tgg cgc ctg tac tcc acc gat atg agc cgg gcc tac ctg     1168
122 Gln Ala Ala Trp Arg Leu Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu
123                 350                 355                 360
125 aca gcc acc tgg tac tac tat gac agt atc ctc cca tcc ttc aga gag     1216
126 Thr Ala Thr Trp Tyr Tyr Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu
127         365                 370                 375
129 ctg gcc ctc ttg ttt gag cac gtg caa cgg gcc cgc aat ggg ggc cta     1264
130 Leu Ala Leu Leu Phe Glu His Val Gln Arg Ala Arg Asn Gly Gly Leu
131     380                 385                 390
133 cgg ccc ctg gag gtg cgg cgg gcg ccg gta ccc gac gga gca ccc tcc     1312
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RAW SEQUENCE LISTING   DATE: 06/26/2001
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134 Arg Pro Leu Glu Val Arg Arg Ala Pro Val Pro Asp Gly Ala Pro Ser
135 395             400             405             410
137 cgt tac ccg ccc gtt gcc acc tgc cac cgg ccg ggc agc acc tcc ttc    1360
138 Arg Tyr Pro Pro Val Ala Thr Cys His Arg Pro Gly Ser Thr Ser Phe
139             415             420             425
141 tgc cct ggg gaa agc agc cgg atg ggc atc aaa gac cgc atc cgc atg    1408
142 Cys Pro Gly Glu Ser Ser Arg Met Gly Ile Lys Asp Arg Ile Arg Met
143             430             435             440
145 ggc agc tcc cag cgg cgg acg ggt cct tcc aag cag cag ctg gca cct    1456
146 Gly Ser Ser Gln Arg Arg Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro
147         445             450             455
149 cca aca atg ccc acc tcc cca agc agc gag cag gtg ggt gag gcc acc    1504
150 Pro Thr Met Pro Thr Ser Pro Ser Ser Glu Gln Val Gly Glu Ala Thr
151     460             465             470
153 agc ccc acc aag gtg caa aag agc tgg agc ttc aat gac cgc acc cgc    1552
154 Ser Pro Thr Lys Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg
155 475             480             485             490
157 ttc cgg gca tct ctg aga ctc aaa ccc cgc acc tct gct gag gat gcc    1600
158 Phe Arg Ala Ser Leu Arg Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala
159             495             500             505
161 ccc tca gag gaa gta gca gag gag aag agc tac cag tgt gag ctc acg    1648
162 Pro Ser Glu Glu Val Ala Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr
163             510             515             520
165 gtg gac gac atc atg cct gct gtg aag aca gtc atc cgc tcc atc agg    1696
166 Val Asp Asp Ile Met Pro Ala Val Lys Thr Val Ile Arg Ser Ile Arg
167         525             530             535
169 att ctc aag ttc ctg gtg gcc aaa agg aaa ttc aag gag aca ctg cga    1744
170 Ile Leu Lys Phe Leu Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg
171     540             545             550
173 ccg tac gac gtg aag gac gtc att gag cag tac tca gca ggc cac ctg    1792
174 Pro Tyr Asp Val Lys Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu
175 555             560             565             570
177 gac atg ctg ggc cgg atc aag agc ctg caa act cgg gtg gac caa att    1840
178 Asp Met Leu Gly Arg Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile
179             575             580             585
181 gtg ggt cgg ggg ccc ggg gac agg aag gcc cgg gag aag ggc gac aag    1888
182 Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys
183             590             595             600
185 ggg ccc tcc gac gcg gag gtg gtg gat gaa atc agc atg atg gga cgc    1936
186 Gly Pro Ser Asp Ala Glu Val Val Asp Glu Ile Ser Met Met Gly Arg
187         605             610             615
189 gtg gtc aag gtg gag aag cag gtg cag tcc atc gag cac aag ctg gac    1984
190 Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu His Lys Leu Asp
191     620             625             630
193 ctg ctg ttg ggc ttc tat tcg cgc tgc ctg cgc tct ggc acc tcg gcc    2032
194 Leu Leu Leu Gly Phe Tyr Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala
195 635             640             645             650
197 agc ctg ggc gcc gtg caa gtg ccg ctg ttc gac ccc gac atc acc tcc    2080
198 Ser Leu Gly Ala Val Gln Val Pro Leu Phe Asp Pro Asp Ile Thr Ser
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199                 655              660                665
201 gac tac cac agc cct gtg gac cac gag gac atc tcc gtc tcc gca cag   2128
202 Asp Tyr His Ser Pro Val Asp His Glu Asp Ile Ser Val Ser Ala Gln
203              670              675              680
205 acg ctc agc atc tcc cgc tcg gtc agc acc aac atg gac tga           2170
206 Thr Leu Ser Ile Ser Arg Ser Val Ser Thr Asn Met Asp
207             685              690              695
209 gggacttctc agaggcaggg cagcacacgg ccagccccgc ggcctggcgc tccgactgcc 2230
211 ctctgaggcc tccggactcc tctcgtactt gaactcactc cctcacgggg agagagacca 2290
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218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens

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224 Asp Ala Pro Arg Ala Glu Leu Val Ala Leu Thr Ala Val Gln Ser Glu
225              20              25              30
226 Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro Arg Arg Leu Gly Leu Leu
227          35              40              45
228 Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu Pro Gly Pro Gly Ser Gly
229      50              55              60
230 Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser Ala Ala His Lys Arg Tyr
231  65              70              75              80
232 Arg Arg Leu Gln Asn Trp Val Tyr Asn Val Leu Glu Arg Pro Arg Gly
233              85              90              95
234 Trp Ala Phe Val Tyr His Val Phe Ile Phe Leu Leu Val Phe Ser Cys
235             100             105             110
236 Leu Val Leu Ser Val Leu Ser Thr Ile Gln Glu His Gln Glu Leu Ala
237          115             120             125
238 Asn Glu Cys Leu Leu Ile Leu Glu Phe Val Met Ile Val Val Phe Gly
239      130             135             140
240 Leu Glu Tyr Ile Val Arg Val Trp Ser Ala Gly Cys Cys Cys Arg Tyr
241 145             150             155             160
242 Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala Arg Lys Pro Phe Cys Val
243             165             170             175
244 Ile Asp Phe Ile Val Phe Val Ala Ser Val Ala Val Ile Ala Ala Gly
245             180             185             190
246 Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala Leu Arg Ser Met Arg Phe
247          195             200             205
248 Leu Gln Ile Leu Arg Met Val Arg Met Asp Arg Arg Gly Gly Thr Trp
249      210             215             220
250 Lys Leu Leu Gly Ser Val Val Tyr Ala His Ser Lys Glu Leu Ile Thr
251 225             230             235             240
252 Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile Phe Ala Ser Phe Leu Val
253             245             250             255
254 Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp Phe Ser Ser Tyr Ala Asp
255             260             265             270
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256 Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp
257      275              280                  285
258 Lys Thr Pro His Thr Trp Leu Gly Arg Val Leu Ala Ala Gly Phe Ala
259      290              295                  300
260 Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser
261 305              310                  315                  320
262 Gly Phe Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe Glu
263              325                  330                  335
264 Lys Arg Arg Met Pro Ala Ala Asn Leu Ile Gln Ala Ala Trp Arg Leu
265              340                  345                  350
266 Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu Thr Ala Thr Trp Tyr Tyr
267      355                  360                  365
268 Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu Leu Ala Leu Leu Phe Glu
269      370                  375                  380
270 His Val Gln Arg Ala Arg Asn Gly Gly Leu Arg Pro Leu Glu Val Arg
271 385              390                  395                  400
272 Arg Ala Pro Val Pro Asp Gly Ala Pro Ser Arg Tyr Pro Pro Val Ala
273              405                  410                  415
274 Thr Cys His Arg Pro Gly Ser Thr Ser Phe Cys Pro Gly Glu Ser Ser
275              420                  425                  430
276 Arg Met Gly Ile Lys Asp Arg Ile Arg Met Gly Ser Ser Gln Arg Arg
277              435                  440                  445
278 Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro Pro Thr Met Pro Thr Ser
279      450                  455                  460
280 Pro Ser Ser Glu Gln Val Gly Glu Ala Thr Ser Pro Thr Lys Val Gln
281 465              470                  475                  480
282 Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Ala Ser Leu Arg
283              485                  490                  495
284 Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala Pro Ser Glu Glu Val Ala
285              500                  505                  510
286 Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr Val Asp Asp Ile Met Pro
287              515                  520                  525
288 Ala Val Lys Thr Val Ile Arg Ser Ile Arg Ile Leu Lys Phe Leu Val
289      530                  535                  540
290 Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys Asp
291 545              550                  555                  560
292 Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile
293              565                  570                  575
294 Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Val Gly Arg Gly Pro Gly
295              580                  585                  590
296 Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys Gly Pro Ser Asp Ala Glu
297              595                  600                  605
298 Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Glu Lys
299      610                  615                  620
300 Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Leu Gly Phe Tyr
301 625              630                  635                  640
302 Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln
303              645                  650                  655
304 Val Pro Leu Phe Asp Pro Asp Ile Thr Ser Asp Tyr His Ser Pro Val
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VERIFICATION SUMMARY
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